

SEQUENCE LISTING

<110> Hoxie, James A.
Lin, George

<120> Compositions, Methods and Kits Relating to Deletion Mutations of
Immunodeficiency Virus gp120 Hypervariable Regions

<130> 053893-5046

<150> 60/443,364
<151> 2003-01-29

<160> 30

<170> PatentIn version 3.2

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<212> DNA
<213> HIV-2/VCP (env)

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 <213> HIV-2/VCP (gp120)

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tgtgacaata acacctcaag tcggagcaag tgttacatga accattgcaa tacatcagtc	600
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gcagaggtgg cagaactata ccgattggaa ttgggagatt acaaattagt agaaatcaca	1440
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caacagctgt tggatgtggt caagaaacaa caagaaatgt tgcgactgac cgtctggga	180
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agagaagaaa cagaagaaga cggttggaaagc aacgggtggag acagatcttgc gcttagccg	720
atagcatata ttcatttcct gatccgcctg ctgattcgcc tcttgatcgg gctatacaac	780
atctgcagag acttactatc caggatctcc ccgatcctcc aaccaatctt ccagagtctc	840
cagagagcac taacagcaat cagagactgg ctgaggctta aagcagccctt cctgcagttat	900
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30	

Pro Ala Trp Arg Asn Ala Ser Ile Pro Leu Phe Cys Ala Thr Lys Asn	
35	40
45	

Arg Asp Thr Trp Gly Thr Ile Gln Cys Leu Pro Asp Asn Asp Asp Tyr

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65								70		75				80	
Thr	Val	Thr	Glu	Gln	Ala	Val	Glu	Asp	Val	Trp	Asn	Leu	Phe	Glu	Thr
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Ser	Ile	Lys	Pro	Cys	Val	Lys	Leu	Thr	Pro	Leu	Cys	Val	Ala	Met	Asn
								100		105				110	
Cys	Thr	Arg	Asn	Met	Thr	Thr	Ser	Thr	Gly	Thr	Thr	Asp	Thr	Gln	Asn
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Ile	Thr	Ile	Ile	Asn	Asp	Thr	Ser	Pro	Cys	Val	Arg	Ala	Asp	Asn	Cys
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Lys	Asp	Val	Ile	Cys	Asp	Asn	Asn	Thr	Ser	Ser	Arg	Ser	Lys	Cys	Tyr
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Met	Asn	His	Cys	Asn	Thr	Ser	Val	Ile	Thr	Glu	Ser	Cys	Asp	Lys	His
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Tyr	Trp	Asp	Ala	Met	Arg	Phe	Arg	Tyr	Cys	Ala	Pro	Pro	Gly	Phe	Ala
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Ser	Lys	Val	Val	Ala	Ala	Thr	Cys	Thr	Arg	Met	Met	Glu	Thr	Gln	Ser
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Ser	Thr	Trp	Phe	Gly	Phe	Asn	Gly	Thr	Arg	Ala	Glu	Asn	Arg	Thr	Tyr
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				275				280			285				

Phe Tyr Asn Leu Thr Met His Cys Lys Arg Pro Gly Asn Lys Thr Val
290 295 300

Leu Pro Ile Met Ser Gly Phe Lys Phe His Ser Lys Pro Val Ile Asn
305 310 315 320

Lys Lys Pro Arg Gln Ala Trp Cys Trp Phe Lys Gly Glu Trp Lys Glu
325 330 335

Ala Met Gln Glu Val Lys Glu Thr Leu Ala Lys His Pro Arg Tyr Lys
340 345 350

Gly Asn Arg Ser Arg Thr Glu Asn Ile Lys Phe Lys Ala Pro Gly Arg
355 360 365

Gly Ser Asp Pro Glu Ala Ala Tyr Met Trp Thr Asn Cys Arg Gly Glu
370 375 380

Phe Leu Tyr Cys Asn Met Thr Trp Phe Leu Asn Trp Val Asp Asn Arg
385 390 395 400

Thr Gly Gln Lys Gln Arg Asn Tyr Ala Pro Cys His Ile Arg Gln Ile
405 410 415

Ile Asn Thr Trp His Arg Val Gly Lys Asn Val Tyr Leu Pro Pro Arg
420 425 430

Glu Gly Glu Leu Thr Cys Asn Ser Thr Val Thr Ser Ile Ile Ala Asn
435 440 445

Ile Asp Thr Gly Asp Gln Thr Asp Ile Thr Phe Ser Ala Glu Val Ala
450 455 460

Glu Leu Tyr Arg Leu Glu Leu Gly Asp Tyr Lys Leu Val Glu Ile Thr
465 470 475 480

Pro Ile Gly Phe Ala Pro Thr Ser Val Lys Arg Tyr Ser Ser Ala His
485 490 495

Gln Arg His Thr Arg Gly Val Phe Val Leu Gly Phe Leu Gly Phe Leu
500 505 510

Ala Thr Ala Gly Ser Ala Met Gly Ala Ala Ser Leu Thr Leu Thr Ala
515 520 525

Gln Ser Arg Thr Ser Leu Ala Gly Ile Val Gln Gln Gln Gln Leu
530 535 540

Leu Asp Val Val Lys Lys Gln Gln Glu Met Leu Arg Leu Thr Val Trp
545 550 555 560

Gly Thr Lys Asn Leu Gln Ala Arg Val Thr Ala Ile Glu Lys Tyr Leu
565 570 575

Lys Asp Gln Ala Gln Leu Asn Ser Trp Gly Cys Ala Phe Arg Gln Val
580 585 590

Cys His Thr Ser Val Pro Trp Val Asn Asp Ser Leu Thr Pro Asp Trp
595 600 605

Asn Asn Met Thr Trp Gln Glu Trp Glu Gln Lys Val Arg Tyr Trp Glu
610 615 620

Ala Asn Ile Ser Gln Ser Leu Glu Gln Ala Gln Ile Gln Gln Glu Lys
625 630 635 640

Asn Leu Tyr Glu Leu Gln Lys Leu Asn Ser Trp Gly Val Phe Thr Asn
645 650 655

Trp Leu Asp Phe Thr Ser Trp Val Arg Tyr Ile Gln Tyr Gly Val Tyr
660 665 670

Val Val Val Gly Ile Val Ala Leu Arg Ile Val Ile Tyr Ile Val Gln
675 680 685

Met Leu Ser Arg Leu Arg Lys Gly Tyr Arg Pro Val Phe Ser Ser Pro
690 695 700

Pro Gly Tyr Ile Gln Gln Ile His Ile His Lys Asp Gln Glu Gln Pro
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Ala Arg Glu Glu Thr Glu Glu Asp Val Gly Ser Asn Gly Gly Asp Arg
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Ser Trp Leu

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<211> 501
<212> PRT
<213> HIV-2/VCP (gp120)

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35 40 45

Arg Asp Thr Trp Gly Thr Ile Gln Cys Leu Pro Asp Asn Asp Asp Tyr
50 55 60

Gln Glu Ile Ala Leu Asn Val Thr Glu Ala Phe Asp Ala Trp Asn Asn
65 70 75 80

Thr Val Thr Glu Gln Ala Val Glu Asp Val Trp Asn Leu Phe Glu Thr
85 90 95

Ser Ile Lys Pro Cys Val Lys Leu Thr Pro Leu Cys Val Ala Met Asn
100 105 110

Cys Thr Arg Asn Met Thr Thr Ser Thr Gly Thr Thr Asp Thr Gln Asn
115 120 125

Ile Thr Ile Ile Asn Asp Thr Ser Pro Cys Val Arg Ala Asp Asn Cys
130 135 140

Thr Gly Leu Lys Glu Glu Glu Met Val Asp Cys Gln Phe Asn Met Thr
145 150 155 160

Gly Leu Glu Arg Asp Lys Arg Lys Gln Tyr Thr Glu Ala Trp Tyr Ser
165 170 175

Lys Asp Val Ile Cys Asp Asn Asn Thr Ser Ser Arg Ser Lys Cys Tyr
180 185 190

Met Asn His Cys Asn Thr Ser Val Ile Thr Glu Ser Cys Asp Lys His
195 200 205

Tyr Trp Asp Ala Met Arg Phe Arg Tyr Cys Ala Pro Pro Gly Phe Ala
210 215 220

Leu Leu Arg Cys Asn Asp Thr Asn Tyr Ser Gly Phe Ala Pro Asn Cys
225 230 235 240

Ser Lys Val Val Ala Ala Thr Cys Thr Arg Met Met Glu Thr Gln Ser
245 250 255

Ser Thr Trp Phe Gly Phe Asn Gly Thr Arg Ala Glu Asn Arg Thr Tyr
260 265 270

Ile Tyr Trp His Gly Lys Asn Asn Arg Thr Ile Ile Ser Leu Asn Asn
275 280 285

Phe Tyr Asn Leu Thr Met His Cys Lys Arg Pro Gly Asn Lys Thr Val
290 295 300

Leu Pro Ile Met Ser Gly Phe Lys Phe His Ser Lys Pro Val Ile Asn
305 310 315 320

Lys Lys Pro Arg Gln Ala Trp Cys Trp Phe Lys Gly Glu Trp Lys Glu
325 330 335

Ala Met Gln Glu Val Lys Glu Thr Leu Ala Lys His Pro Arg Tyr Lys
340 345 350

Gly Asn Arg Ser Arg Thr Glu Asn Ile Lys Phe Lys Ala Pro Gly Arg
355 360 365

Gly Ser Asp Pro Glu Ala Ala Tyr Met Trp Thr Asn Cys Arg Gly Glu
370 375 380

Phe Leu Tyr Cys Asn Met Thr Trp Phe Leu Asn Trp Val Asp Asn Arg
385 390 395 400

Thr Gly Gln Lys Gln Arg Asn Tyr Ala Pro Cys His Ile Arg Gln Ile
405 410 415

Ile Asn Thr Trp His Arg Val Gly Lys Asn Val Tyr Leu Pro Pro Arg
420 425 430

Glu Gly Glu Leu Thr Cys Asn Ser Thr Val Thr Ser Ile Ile Ala Asn
435 440 445

Ile Asp Thr Gly Asp Gln Thr Asp Ile Thr Phe Ser Ala Glu Val Ala
450 455 460

Glu Leu Tyr Arg Leu Glu Leu Gly Asp Tyr Lys Leu Val Glu Ile Thr
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Pro Ile Gly Phe Ala Pro Thr Ser Val Lys Arg Tyr Ser Ser Ala His
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Gln Arg His Thr Arg
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<212> PRT
<213> HIV-2/VCP (gp41)

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35 40 45

Lys Gln Gln Glu Met Leu Arg Leu Thr Val Trp Gly Thr Lys Asn Leu
50 55 60

Gln Ala Arg Val Thr Ala Ile Glu Lys Tyr Leu Lys Asp Gln Ala Gln
65 70 75 80

Leu Asn Ser Trp Gly Cys Ala Phe Arg Gln Val Cys His Thr Ser Val
85 90 95

Pro Trp Val Asn Asp Ser Leu Thr Pro Asp Trp Asn Asn Met Thr Trp

100 105 110

Gln Glu Trp Glu Gln Lys Val Arg Tyr Trp Glu Ala Asn Ile Ser Gln
115 120 125

Ser Leu Glu Gln Ala Gln Ile Gln Gln Glu Lys Asn Leu Tyr Glu Leu
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Gln Lys Leu Asn Ser Trp Gly Val Phe Thr Asn Trp Leu Asp Phe Thr
145 150 155 160

Ser Trp Val Arg Tyr Ile Gln Tyr Gly Val Tyr Val Val Val Gly Ile
165 170 175

Val Ala Leu Arg Ile Val Ile Tyr Ile Val Gln Met Leu Ser Arg Leu
180 185 190

Arg Lys Gly Tyr Arg Pro Val Phe Ser Ser Pro Pro Gly Tyr Ile Gln
195 200 205

Gln Ile His Ile His Lys Asp Gln Glu Gln Pro Ala Arg Glu Glu Thr
210 215 220

Glu Glu Asp Val Gly Ser Asn Gly Gly Asp Arg Ser Trp Leu Pro Ile
225 230 235 240

Ala Tyr Ile His Phe Leu Ile Arg Leu Leu Ile Arg Leu Leu Ile Gly
245 250 255

Leu Tyr Asn Ile Cys Arg Asp Leu Leu Ser Arg Ile Ser Pro Ile Leu
260 265 270

Gln Pro Ile Phe Gln Ser Leu Gln Arg Ala Leu Thr Ala Ile Arg Asp
275 280 285

Trp Leu Arg Leu Lys Ala Ala Tyr Leu Gln Tyr Gly Cys Glu Trp Ile
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gagactcttg caggcgcggg g	2181

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 <212> DNA
 <213> HIV-2/VCP Clone p16.5 (gp120)

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ccccctgtttt gtgcaaccaa aaatagagat acttggggaa ctgtacagtg cttgccagac	180
aatgatgatt atcagaaaaat agctttaaat gtaacagagg ctttcgatgc atggataat	240
acagtaacag aacaagcagt ggaggatgtc tggaaatctat ttgagacatc aataaaacca	300
tgtgtcaaatt taacaccctt atgtgttaggt gcccgcatt gcaatacatc agtcatcaaa	360
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aatggcacta gaacagaaaa tagaacatata atctattggc atggtaaaaa taacagaact	600
attatcagct taaataactt ttataatctc actatgcatt gtaagaggcc gggaaataag	660
ggtgcggca aacccaggca agcatgggtgt tggttcaaag gcgaatggaa ggaagccatg	720
caggaggtga aggagaccct tgcgaaacat cccagatata aagggaaacag gagccgcaca	780

gagaatatta aatttaaagc accaggaaga ggctcagacc cagaagcagc atacatgtgg 840
actaactgca gagggaaatt tctctactgc gacatgactt ggttcctcaa ttgggttagat 900
aacaggacgg gtcagaaaca gcgcattat gcaccgtgcc atataagaca aataattaat 960
acttggcaca gggtagggaa aaacgtataat ttgcctccca gggagggga gttgacctgc 1020
aactcaacag tgaccagcat aattgccaac attgatacgg gagatcaaac agatattacc 1080
tttagtgcag aggtggcaga actataccga ttgaaattgg gagattacaa attagtagaa 1140
atcacaccaa ttggcttcgc acctacatca gtaaagagat actcctctgc tcaccagaga 1200
catacaaga 1209

<210> 9
<211> 972
<212> DNA
<213> HIV-2/VCP Clone p16.5 (gp41)

<400> 9
ggtgtgttcg tgctagggtt ctgggtttt ctgcacacgg caggttctgc aatggcgcg 60
gcgtcggtga cgctgaccgc tcagtcggg acttcattga ctggatagt gcagcaacag 120
caacagctgt tggatgtggt caagaaacaa caagaaatgt tgcgactgac cgtctgggg 180
actaaaaatc tccaggcaag agtcactgct atagagaaaat acctaaagga ccaggcgcag 240
ctaaattcat gggatgtgc gtttagacaa gtctgccaca cttctgtacc atggtaaat 300
gatacgcttga cacctgattt gaacaatatg acgtggcagg aatggaaaca aaaagtccgc 360
tactgggagg caaatatcag tcaaagtcta gaacaagcac aaattcagca agaaaagaat 420
ttgtatgagc tgcaaaaatt aaatagctgg ggtgtttta ccaattggct tgacttcacc 480
tcctgggtca ggtatattca atatggagtt tacgttagtag taggaatagt agctttaaga 540
atagtaatat atatagtaca gatgttaagt agacttagga agggctatacg gcctgtttc 600
tcctcccccc ccggttatat ccaacagatc catatccaca aggaccagga acagccagcc 660
agagaagaaa cagaagaaga cgttggaaagc aacggtgag acagatctg gcttagccg 720
atagcatata ttcatatcct gatccgcctg ctgattcgcc tcttgatcgg gctatacaac 780
atctgcagag acttactatc caggatctcc ccgatcctcc aaccaatctt ccagagtctc 840
cagagagcac taacagcaat cagagactgg ctgaggctt aagcagccctt cctgcagtat 900
gggtgcgagt ggatccaaga agcgttccaa gcccttgcaa ggactacaag agagactctt 960
gcaggcgcgg gg 972

<210> 10
<211> 726
<212> PRT
<213> HIV-2/VCP Clone p16.5 (env)

<400> 10

Met Lys Gly Ser Lys Asn Gln Leu Leu Ile Ala Ile Val Leu Ala Ser
1 5 10 15

Ala Tyr Leu Thr His Cys Lys Gln Phe Val Thr Val Phe Tyr Gly Ile
20 25 30

Pro Ala Trp Arg Asn Ala Ser Ile Pro Leu Phe Cys Ala Thr Lys Asn
35 40 45

Arg Asp Thr Trp Gly Thr Val Gln Cys Leu Pro Asp Asn Asp Asp Tyr
50 55 60

Gln Glu Ile Ala Leu Asn Val Thr Glu Ala Phe Asp Ala Trp Asp Asn
65 70 75 80

Thr Val Thr Glu Gln Ala Val Glu Asp Val Trp Asn Leu Phe Glu Thr
85 90 95

Ser Ile Lys Pro Cys Val Lys Leu Thr Pro Leu Cys Val Gly Ala Gly
100 105 110

His Cys Asn Thr Ser Val Ile Lys Glu Ser Cys Asp Lys His Tyr Trp
115 120 125

Asp Ala Met Arg Phe Arg Tyr Cys Ala Pro Pro Gly Phe Ala Leu Leu
130 135 140

Arg Cys Asn Asp Ile Asn Tyr Ser Gly Phe Ala Pro Asn Cys Ser Lys
145 150 155 160

Val Val Ala Ala Thr Cys Thr Arg Met Met Glu Thr Gln Ser Ser Thr
165 170 175

Trp Phe Gly Phe Asn Gly Thr Arg Thr Glu Asn Arg Thr Tyr Ile Tyr
180 185 190

Trp His Gly Lys Asn Asn Arg Thr Ile Ile Ser Leu Asn Asn Phe Tyr
195 200 205

Asn Leu Thr Met His Cys Lys Arg Pro Gly Asn Lys Gly Ala Gly Lys
210 215 220

Pro Arg Gln Ala Trp Cys Trp Phe Lys Gly Glu Trp Lys Glu Ala Met
225 230 235 240

Gln Glu Val Lys Glu Thr Leu Ala Lys His Pro Arg Tyr Lys Gly Asn
245 250 255

Arg Ser Arg Thr Glu Asn Ile Lys Phe Lys Ala Pro Gly Arg Gly Ser
260 265 270

Asp Pro Glu Ala Ala Tyr Met Trp Thr Asn Cys Arg Gly Glu Phe Leu
275 280 285

Tyr Cys Asp Met Thr Trp Phe Leu Asn Trp Val Asp Asn Arg Thr Gly
290 295 300

Gln Lys Gln Arg Asn Tyr Ala Pro Cys His Ile Arg Gln Ile Ile Asn
305 310 315 320

Thr Trp His Arg Val Gly Lys Asn Val Tyr Leu Pro Pro Arg Glu Gly
325 330 335

Glu Leu Thr Cys Asn Ser Thr Val Thr Ser Ile Ile Ala Asn Ile Asp
340 345 350

Thr Gly Asp Gln Thr Asp Ile Thr Phe Ser Ala Glu Val Ala Glu Leu
355 360 365

Tyr Arg Leu Glu Leu Gly Asp Tyr Lys Leu Val Glu Ile Thr Pro Ile
370 375 380

Gly Phe Ala Pro Thr Ser Val Lys Arg Tyr Ser Ser Ala His Gln Arg
385 390 395 400

His Thr Arg Gly Val Phe Val Leu Gly Phe Leu Gly Phe Leu Ala Thr
405 410 415

Ala Gly Ser Ala Met Gly Ala Ala Ser Val Thr Leu Thr Ala Gln Ser

420

425

430

Arg Thr Ser Leu Thr Gly Ile Val Gln Gln Gln Gln Gln Leu Leu Asp
435 440 445

Val Val Lys Lys Gln Gln Glu Met Leu Arg Leu Thr Val Trp Gly Thr
450 455 460

Lys Asn Leu Gln Ala Arg Val Thr Ala Ile Glu Lys Tyr Leu Lys Asp
465 470 475 480

Gln Ala Gln Leu Asn Ser Trp Gly Cys Ala Phe Arg Gln Val Cys His
485 490 495

Thr Ser Val Pro Trp Val Asn Asp Ser Leu Thr Pro Asp Trp Asn Asn
500 505 510

Met Thr Trp Gln Glu Trp Glu Gln Lys Val Arg Tyr Trp Glu Ala Asn
515 520 525

Ile Ser Gln Ser Leu Glu Gln Ala Gln Ile Gln Gln Glu Lys Asn Leu
530 535 540

Tyr Glu Leu Gln Lys Leu Asn Ser Trp Gly Val Phe Thr Asn Trp Leu
545 550 555 560

Asp Phe Thr Ser Trp Val Arg Tyr Ile Gln Tyr Gly Val Tyr Val Val
565 570 575

Val Gly Ile Val Ala Leu Arg Ile Val Ile Tyr Ile Val Gln Met Leu
580 585 590

Ser Arg Leu Arg Lys Gly Tyr Arg Pro Val Phe Ser Ser Pro Pro Gly
595 600 605

Tyr Ile Gln Gln Ile His Ile His Lys Asp Gln Glu Gln Pro Ala Arg
610 615 620

Glu Glu Thr Glu Glu Asp Val Gly Ser Asn Gly Gly Asp Arg Ser Trp
625 630 635 640

Leu Pro Ile Ala Tyr Ile His Phe Leu Ile Arg Leu Leu Ile Arg Leu
645 650 655

Leu Ile Gly Leu Tyr Asn Ile Cys Arg Asp Leu Leu Ser Arg Ile Ser
660 665 670

Pro Ile Leu Gln Pro Ile Phe Gln Ser Leu Gln Arg Ala Leu Thr Ala
675 680 685

Ile Arg Asp Trp Leu Arg Leu Lys Ala Ala Tyr Leu Gln Tyr Gly Cys
690 695 700

Glu Trp Ile Gln Glu Ala Phe Gln Ala Leu Ala Arg Thr Thr Arg Glu
705 710 715 720

Thr Leu Ala Gly Ala Gly
725

<210> 11
<211> 403
<212> PRT
<213> HIV-2/VCP Clone p16.5 (gp120)

<400> 11

Met Lys Gly Ser Lys Asn Gln Leu Leu Ile Ala Ile Val Leu Ala Ser
1 5 10 15

Ala Tyr Leu Thr His Cys Lys Gln Phe Val Thr Val Phe Tyr Gly Ile
20 25 30

Pro Ala Trp Arg Asn Ala Ser Ile Pro Leu Phe Cys Ala Thr Lys Asn
35 40 45

Arg Asp Thr Trp Gly Thr Val Gln Cys Leu Pro Asp Asn Asp Asp Tyr
50 55 60

Gln Glu Ile Ala Leu Asn Val Thr Glu Ala Phe Asp Ala Trp Asp Asn
65 70 75 80

Thr Val Thr Glu Gln Ala Val Glu Asp Val Trp Asn Leu Phe Glu Thr
85 90 95

Ser Ile Lys Pro Cys Val Lys Leu Thr Pro Leu Cys Val Gly Ala Gly
100 105 110

His Cys Asn Thr Ser Val Ile Lys Glu Ser Cys Asp Lys His Tyr Trp
115 120 125

Asp Ala Met Arg Phe Arg Tyr Cys Ala Pro Pro Gly Phe Ala Leu Leu
130 135 140

Arg Cys Asn Asp Ile Asn Tyr Ser Gly Phe Ala Pro Asn Cys Ser Lys
145 150 155 160

Val Val Ala Ala Thr Cys Thr Arg Met Met Glu Thr Gln Ser Ser Thr
165 170 175

Trp Phe Gly Phe Asn Gly Thr Arg Thr Glu Asn Arg Thr Tyr Ile Tyr
180 185 190

Trp His Gly Lys Asn Asn Arg Thr Ile Ile Ser Leu Asn Asn Phe Tyr
195 200 205

Asn Leu Thr Met His Cys Lys Arg Pro Gly Asn Lys Gly Ala Gly Lys
210 215 220

Pro Arg Gln Ala Trp Cys Trp Phe Lys Gly Glu Trp Lys Glu Ala Met
225 230 235 240

Gln Glu Val Lys Glu Thr Leu Ala Lys His Pro Arg Tyr Lys Gly Asn
245 250 255

Arg Ser Arg Thr Glu Asn Ile Lys Phe Lys Ala Pro Gly Arg Gly Ser
260 265 270

Asp Pro Glu Ala Ala Tyr Met Trp Thr Asn Cys Arg Gly Glu Phe Leu
275 280 285

Tyr Cys Asp Met Thr Trp Phe Leu Asn Trp Val Asp Asn Arg Thr Gly
290 295 300

Gln Lys Gln Arg Asn Tyr Ala Pro Cys His Ile Arg Gln Ile Ile Asn
305 310 315 320

Thr Trp His Arg Val Gly Lys Asn Val Tyr Leu Pro Pro Arg Glu Gly
325 330 335

Glu Leu Thr Cys Asn Ser Thr Val Thr Ser Ile Ile Ala Asn Ile Asp

340

345

350

Thr Gly Asp Gln Thr Asp Ile Thr Phe Ser Ala Glu Val Ala Glu Leu
355 360 365

Tyr Arg Leu Glu Leu Gly Asp Tyr Lys Leu Val Glu Ile Thr Pro Ile
370 375 380

Gly Phe Ala Pro Thr Ser Val Lys Arg Tyr Ser Ser Ala His Gln Arg
385 390 395 400

His Thr Arg

<210> 12
<211> 323
<212> PRT
<213> HIV-2/VCP Clone p16.5 (gp41)

<400> 12

Gly Val Phe Val Leu Gly Phe Leu Gly Phe Leu Ala Thr Ala Gly Ser
1 5 10 15

Ala Met Gly Ala Ala Ser Val Thr Leu Thr Ala Gln Ser Arg Thr Ser
20 25 30

Leu Thr Gly Ile Val Gln Gln Gln Gln Leu Leu Asp Val Val Lys
35 40 45

Lys Gln Gln Glu Met Leu Arg Leu Thr Val Trp Gly Thr Lys Asn Leu
50 55 60

Gln Ala Arg Val Thr Ala Ile Glu Lys Tyr Leu Lys Asp Gln Ala Gln
65 70 75 80

Leu Asn Ser Trp Gly Cys Ala Phe Arg Gln Val Cys His Thr Ser Val
85 90 95

Pro Trp Val Asn Asp Ser Leu Thr Pro Asp Trp Asn Asn Met Thr Trp
100 105 110

Gln Glu Trp Glu Gln Lys Val Arg Tyr Trp Glu Ala Asn Ile Ser Gln
115 120 125

Ser Leu Glu Gln Ala Gln Ile Gln Gln Glu Lys Asn Leu Tyr Glu Leu
130 135 140

Gln Lys Leu Asn Ser Trp Gly Val Phe Thr Asn Trp Leu Asp Phe Thr
145 150 155 160

Ser Trp Val Arg Tyr Ile Gln Tyr Gly Val Tyr Val Val Val Gly Ile
165 170 175

Val Ala Leu Arg Ile Val Ile Tyr Ile Val Gln Met Leu Ser Arg Leu
180 185 190

Arg Lys Gly Tyr Arg Pro Val Phe Ser Ser Pro Pro Gly Tyr Ile Gln
195 200 205

Gln Ile His Ile His Lys Asp Gln Glu Gln Pro Ala Arg Glu Glu Thr
210 215 220

Glu Glu Asp Val Gly Ser Asn Gly Gly Asp Arg Ser Trp Leu Pro Ile
225 230 235 240

Ala Tyr Ile His Phe Leu Ile Arg Leu Leu Ile Arg Leu Leu Ile Gly
245 250 255

Leu Tyr Asn Ile Cys Arg Asp Leu Leu Ser Arg Ile Ser Pro Ile Leu
260 265 270

Gln Pro Ile Phe Gln Ser Leu Gln Arg Ala Leu Thr Ala Ile Arg Asp
275 280 285

Trp Leu Arg Leu Lys Ala Ala Tyr Leu Gln Tyr Gly Cys Glu Trp Ile
290 295 300

Gln Glu Ala Phe Gln Ala Leu Ala Arg Thr Thr Arg Glu Thr Leu Ala
305 310 315 320

Gly Ala Gly

<210> 13
<211> 1926
<212> DNA
<213> HIV-2/VCP Clone p16.7 (env)

<400> 13
 atgaagggta gtaagaatca accgctgatt gctattgtac tagctagtgc ttacctaaca 60
 cattgcaagc aatttgtgac tgttttctat ggcatacccg cgtggaggaa tgcattccatt 120
 cccctgtttt gtgcaaccaa aaatagagat acttggggaa ccgtacagtg cttgccagac 180
 aatgatgatt atcagggaaat agctttaaat gtaacagagg ctttcgatgc atggataat 240
 acagtaacag aacaaggcagt ggaggatgtc tggaaatctat ctgagacatc aataaaacca 300
 tgtgtcaaatt taacaccctt atgtgttaggt gccggccatt gcaatacatc agtcatcaca 360
 gagtcatgtg ataagcacta ttgggatgct atgaggttta gatactgtgc accaccgggt 420
 tttgccttac taagatgcaa tgatactaattattcaggct ttgcacctaa ttgcctaa 480
 gtagtagctg ctacatgcac cagaatgatg gaaacgcaat cttctacatg gtttggctt 540
 aatggcacta gagcagaaaa tagaacatatacttatttggc atggtaaaaa tgacagaact 600
 attatcagct taaataactt ttataatctc actatgcatt gtaagaggcc gggaaataag 660
 ggtgccggca aacccaggca agcatgggt tggttcaaag gcgaatggaa ggaagccatg 720
 caggaggtga aggagaccct tgcgaaacat cctagatata aagggAACAG gagccgcaca 780
 gagaatatta aattttaaagc accaggaaga ggctcagacc cagaaggcagc atacatgtgg 840
 actaactgca gaggggaaatt tctctactgc gacatgactt gggttctcaa ttgggttagaa 900
 aacaggacgg gtcagaaaca gcgttaattat gcaccgtgcc atataaggca aataattaat 960
 acttggcaca gggtagggaa aaacgtataat ttgcctccca gggagggaa gttaacctgc 1020
 aactcaacag tgaccagcat aattgccaac attgatacgg gagatcaaac agatattacc 1080
 ttttagtgcag aggtggcaga actataccgg ttggaaattgg gagattacaa attagtagaa 1140
 atcacaccaa ttggcttcgc acctacatca gtaaagagat actcctctgc tcaccagaga 1200
 catacaagag gtgtgttcgt gctagggttc ttgggttttc tcgcaacggc aggttctgca 1260
 atgggcgcgg cgtcggtgac gctgaccgct cagtcggcga cttcattgac tgggttagtg 1320
 cagcaacagc aacagctgtt ggatgtggc aagaaacaac aagaaatgtt gcgactgacc 1380
 gtctggggaa ctaaaaatct ccaggcaaga gtcactgcta tagagaaata cctaaaggac 1440
 caggcgcagc taaattcatg gggatgtgcg ttttagacaag tctgccacac ttctgtacca 1500
 tgggtaaatg atagcttgac acctgattgg aacaatatga cgtggcagga atgggaacaa 1560
 aaagtccgct actgggaggc aaatatcagt caaagtctag aacaaggcaca aattcagcaa 1620
 gaaaagaatt tgtatgagct gcaaaaatata aatagctggg gtgttttac caattggctt 1680

gacttcacct cctgggtcag gtatattcaa tatggagttt atgttagtagt aggaatagta	1740
gctttaagaa tagtaatata tatagtacag atgttgagta gacttaggaa gggctatagg	1800
cctgtttct cctccccccc cggttatatc caacagatcc atatccacaa ggaccaggaa	1860
cagccagcca gagaagaaac agaagaagac gttggaagca acggtgagaa caaatcttgg	1920
ctttag	1926

<210> 14
 <211> 1209
 <212> DNA
 <213> HIV-2/VCP Clone p16.7 (gp120)

<400> 14	
atgaaggta gtaagaatca accgctgatt gctattgtac tagctagtgc ttacctaaca	60
cattgcaagc aatttgcac tgggttctat ggcatacccg cgtggaggaa tgcattccatt	120
ccctgtttt gtgcaaccaa aaatagagat acttggggaa ccgtacagtg cttgccagac	180
aatgatgatt atcagggaaat agctttaaat gtaacagagg ctttcgatgc atggataat	240
acagtaacag aacaaggcagt ggaggatgtc tggaaatctat ctgagacatc aataaaacca	300
tgtgtcaaatt taacaccctt atgtgttaggt gccggccatt gcaatacatc agtcatcaca	360
gagtcatgtg ataagcacta ttgggatgtc atgaggttta gatactgtgc accaccgggt	420
tttgccttac taagatgcaa tgataactaat tattcaggct ttgcaccaa ttgctctaaa	480
gttagtagctg ctacatgcac cagaatgtat gaaacgcaat cttctacatg gttggcttt	540
aatggcacta gagcagaaaa tagaacatata atctattggc atggtaaaaa tgacagaact	600
attatcagct taaataactt ttataatctc actatgcatt gtaagaggcc gggaaataag	660
ggtgccggca aaccaggca agcatgggt tggttcaaag gcgaatggaa ggaagccatg	720
caggaggta aggagaccct tgcgaaacat cctagatata aagggacag gagccgcaca	780
gagaatatta aatttaaagc accaggaaga ggctcagacc cagaacgcac atacatgtgg	840
actaactgca gagggaaatt tctctactgc gacatgactt gttcctcaa ttggtagaa	900
aacaggacgg gtcagaaaca gcgttaattat gcaccgtgcc atataaggca aataattaat	960
acttggcaca gggtagggaa aaacgtataat ttgcctccca gggaaaggaa gttaacctgc	1020
aactcaacag tgaccagcat aattgccaac attgatacgg gagatcaaac agatattacc	1080
tttagtgcag aggtggcaga actataccgg ttggaattgg gagattacaa attagtagaa	1140
atcacaccaa ttggcttcgc acctacatca gtaaagagat actcctctgc tcaccagaga	1200

catacaaga 1209

<210> 15
<211> 717
<212> DNA
<213> HIV-2/VCP Clone p16.7 (gp41)

<400> 15
ggtgtgttcg tgctagggtt cttgggtttt ctcgcaacgg caggttctgc aatgggcgcg 60
gcgtcggtga cgctgaccgc tcagtcggc acttcattga ctggggtagt gcagcaacag 120
caacagctgt tggatgtggt caagaaacaa caagaaatgt tgcgactgac cgtctgggga 180
actaaaaatc tccaggcaag agtcactgct atagagaaat acctaaagga ccaggcgcag 240
ctaaattcat gggatgtgc gtttagacaa gtctgccaca cttctgtacc atgggtaaat 300
gatagcttga cacctgattt gaacaatatg acgtggcagg aatgggaaca aaaagtccgc 360
tactgggagg caaatatcag tcaaagtcta gaacaagcac aaattcagca agaaaagaat 420
ttgtatgagc tgcaaaaatt aaatagctgg ggtgtttta ccaattggct tgacttcacc 480
tcctgggtca ggtatattca atatggagtt tatgttagtag taggaatagt agctttaaga 540
atagtaatat atatagtaca gatgttgagt agacttagga agggctatacg gcctgtttc 600
tcctcccccc ccggttatat ccaacagatc catatccaca aggaccagga acagccagcc 660
agagaagaaa cagaagaaga cggttggaaagc aacgggtggag acaaatcttgc gcttttag 717

<210> 16
<211> 641
<212> PRT
<213> HIV-2/VCP Clone p16.7 (env)

<400> 16

Met Lys Gly Ser Lys Asn Gln Pro Leu Ile Ala Ile Val Leu Ala Ser
1 5 10 15

Ala Tyr Leu Thr His Cys Lys Gln Phe Val Thr Val Phe Tyr Gly Ile
20 25 30

Pro Ala Trp Arg Asn Ala Ser Ile Pro Leu Phe Cys Ala Thr Lys Asn
35 40 45

Arg Asp Thr Trp Gly Thr Val Gln Cys Leu Pro Asp Asn Asp Asp Tyr
50 55 60

Gln Glu Ile Ala Leu Asn Val Thr Glu Ala Phe Asp Ala Trp Asp Asn
65 70 75 80

Thr Val Thr Glu Gln Ala Val Glu Asp Val Trp Asn Leu Ser Glu Thr
85 90 95

Ser Ile Lys Pro Cys Val Lys Leu Thr Pro Leu Cys Val Gly Ala Gly
100 105 110

His Cys Asn Thr Ser Val Ile Thr Glu Ser Cys Asp Lys His Tyr Trp
115 120 125

Asp Ala Met Arg Phe Arg Tyr Cys Ala Pro Pro Gly Phe Ala Leu Leu
130 135 140

Arg Cys Asn Asp Thr Asn Tyr Ser Gly Phe Ala Pro Asn Cys Ser Lys
145 150 155 160

Val Val Ala Ala Thr Cys Thr Arg Met Met Glu Thr Gln Ser Ser Thr
165 170 175

Trp Phe Gly Phe Asn Gly Thr Arg Ala Glu Asn Arg Thr Tyr Ile Tyr
180 185 190

Trp His Gly Lys Asn Asp Arg Thr Ile Ile Ser Leu Asn Asn Phe Tyr
195 200 205

Asn Leu Thr Met His Cys Lys Arg Pro Gly Asn Lys Gly Ala Gly Lys
210 215 220

Pro Arg Gln Ala Trp Cys Trp Phe Lys Gly Glu Trp Lys Glu Ala Met
225 230 235 240

Gln Glu Val Lys Glu Thr Leu Ala Lys His Pro Arg Tyr Lys Gly Asn
245 250 255

Arg Ser Arg Thr Glu Asn Ile Lys Phe Lys Ala Pro Gly Arg Gly Ser
260 265 270

Asp Pro Glu Ala Ala Tyr Met Trp Thr Asn Cys Arg Gly Glu Phe Leu
275 280 285

Tyr Cys Asp Met Thr Trp Phe Leu Asn Trp Val Glu Asn Arg Thr Gly
290 295 300

Gln Lys Gln Arg Asn Tyr Ala Pro Cys His Ile Arg Gln Ile Ile Asn
305 310 315 320

Thr Trp His Arg Val Gly Lys Asn Val Tyr Leu Pro Pro Arg Glu Gly
325 330 335

Glu Leu Thr Cys Asn Ser Thr Val Thr Ser Ile Ile Ala Asn Ile Asp
340 345 350

Thr Gly Asp Gln Thr Asp Ile Thr Phe Ser Ala Glu Val Ala Glu Leu
355 360 365

Tyr Arg Leu Glu Leu Gly Asp Tyr Lys Leu Val Glu Ile Thr Pro Ile
370 375 380

Gly Phe Ala Pro Thr Ser Val Lys Arg Tyr Ser Ser Ala His Gln Arg
385 390 395 400

His Thr Arg Gly Val Phe Val Leu Gly Phe Leu Gly Phe Leu Ala Thr
405 410 415

Ala Gly Ser Ala Met Gly Ala Ala Ser Val Thr Leu Thr Ala Gln Ser
420 425 430

Arg Thr Ser Leu Thr Gly Val Val Gln Gln Gln Gln Leu Leu Asp
435 440 445

Val Val Lys Lys Gln Gln Glu Met Leu Arg Leu Thr Val Trp Gly Thr
450 455 460

Lys Asn Leu Gln Ala Arg Val Thr Ala Ile Glu Lys Tyr Leu Lys Asp
465 470 475 480

Gln Ala Gln Leu Asn Ser Trp Gly Cys Ala Phe Arg Gln Val Cys His
485 490 495

Thr Ser Val Pro Trp Val Asn Asp Ser Leu Thr Pro Asp Trp Asn Asn
500 505 510

Met Thr Trp Gln Glu Trp Glu Gln Lys Val Arg Tyr Trp Glu Ala Asn

515

520

525

Ile Ser Gln Ser Leu Glu Gln Ala Gln Ile Gln Gln Glu Lys Asn Leu
530 535 540

Tyr Glu Leu Gln Lys Leu Asn Ser Trp Gly Val Phe Thr Asn Trp Leu
545 550 555 560

Asp Phe Thr Ser Trp Val Arg Tyr Ile Gln Tyr Gly Val Tyr Val Val
565 570 575

Val Gly Ile Val Ala Leu Arg Ile Val Ile Tyr Ile Val Gln Met Leu
580 585 590

Ser Arg Leu Arg Lys Gly Tyr Arg Pro Val Phe Ser Ser Pro Pro Gly
595 600 605

Tyr Ile Gln Gln Ile His Ile His Lys Asp Gln Glu Gln Pro Ala Arg
610 615 620

Glu Glu Thr Glu Glu Asp Val Gly Ser Asn Gly Gly Asp Lys Ser Trp
625 630 635 640

Leu

<210> 17
<211> 403
<212> PRT
<213> HIV-2/VCP Clone p16.7 (gp120)

<400> 17

Met Lys Gly Ser Lys Asn Gln Pro Leu Ile Ala Ile Val Leu Ala Ser
1 5 10 15

Ala Tyr Leu Thr His Cys Lys Gln Phe Val Thr Val Phe Tyr Gly Ile
20 25 30

Pro Ala Trp Arg Asn Ala Ser Ile Pro Leu Phe Cys Ala Thr Lys Asn
35 40 45

Arg Asp Thr Trp Gly Thr Val Gln Cys Leu Pro Asp Asn Asp Asp Tyr
50 55 60

Gln Glu Ile Ala Leu Asn Val Thr Glu Ala Phe Asp Ala Trp Asp Asn
65 70 75 80

Thr Val Thr Glu Gln Ala Val Glu Asp Val Trp Asn Leu Ser Glu Thr
85 90 95

Ser Ile Lys Pro Cys Val Lys Leu Thr Pro Leu Cys Val Gly Ala Gly
100 105 110

His Cys Asn Thr Ser Val Ile Thr Glu Ser Cys Asp Lys His Tyr Trp
115 120 125

Asp Ala Met Arg Phe Arg Tyr Cys Ala Pro Pro Gly Phe Ala Leu Leu
130 135 140

Arg Cys Asn Asp Thr Asn Tyr Ser Gly Phe Ala Pro Asn Cys Ser Lys
145 150 155 160

Val Val Ala Ala Thr Cys Thr Arg Met Met Glu Thr Gln Ser Ser Thr
165 170 175

Trp Phe Gly Phe Asn Gly Thr Arg Ala Glu Asn Arg Thr Tyr Ile Tyr
180 185 190

Trp His Gly Lys Asn Asp Arg Thr Ile Ile Ser Leu Asn Asn Phe Tyr
195 200 205

Asn Leu Thr Met His Cys Lys Arg Pro Gly Asn Lys Gly Ala Gly Lys
210 215 220

Pro Arg Gln Ala Trp Cys Trp Phe Lys Gly Glu Trp Lys Glu Ala Met
225 230 235 240

Gln Glu Val Lys Glu Thr Leu Ala Lys His Pro Arg Tyr Lys Gly Asn
245 250 255

Arg Ser Arg Thr Glu Asn Ile Lys Phe Lys Ala Pro Gly Arg Gly Ser
260 265 270

Asp Pro Glu Ala Ala Tyr Met Trp Thr Asn Cys Arg Gly Glu Phe Leu
275 280 285

Tyr Cys Asp Met Thr Trp Phe Leu Asn Trp Val Glu Asn Arg Thr Gly
290 295 300

Gln Lys Gln Arg Asn Tyr Ala Pro Cys His Ile Arg Gln Ile Ile Asn
305 310 315 320

Thr Trp His Arg Val Gly Lys Asn Val Tyr Leu Pro Pro Arg Glu Gly
325 330 335

Glu Leu Thr Cys Asn Ser Thr Val Thr Ser Ile Ile Ala Asn Ile Asp
340 345 350

Thr Gly Asp Gln Thr Asp Ile Thr Phe Ser Ala Glu Val Ala Glu Leu
355 360 365

Tyr Arg Leu Glu Leu Gly Asp Tyr Lys Leu Val Glu Ile Thr Pro Ile
370 375 380

Gly Phe Ala Pro Thr Ser Val Lys Arg Tyr Ser Ser Ala His Gln Arg
385 390 395 400

His Thr Arg

<210> 18
<211> 238
<212> PRT
<213> HIV-2/VCP Clone p16.7 (gp41)

<400> 18

Gly Val Phe Val Leu Gly Phe Leu Gly Phe Leu Ala Thr Ala Gly Ser
1 5 10 15

Ala Met Gly Ala Ala Ser Val Thr Leu Thr Ala Gln Ser Arg Thr Ser
20 25 30

Leu Thr Gly Val Val Gln Gln Gln Gln Leu Leu Asp Val Val Lys
35 40 45

Lys Gln Gln Glu Met Leu Arg Leu Thr Val Trp Gly Thr Lys Asn Leu
50 55 60

Gln Ala Arg Val Thr Ala Ile Glu Lys Tyr Leu Lys Asp Gln Ala Gln
65 70 75 80

Leu Asn Ser Trp Gly Cys Ala Phe Arg Gln Val Cys His Thr Ser Val
85 90 95

Pro Trp Val Asn Asp Ser Leu Thr Pro Asp Trp Asn Asn Met Thr Trp
100 105 110

Gln Glu Trp Glu Gln Lys Val Arg Tyr Trp Glu Ala Asn Ile Ser Gln
115 120 125

Ser Leu Glu Gln Ala Gln Ile Gln Gln Glu Lys Asn Leu Tyr Glu Leu
130 135 140

Gln Lys Leu Asn Ser Trp Gly Val Phe Thr Asn Trp Leu Asp Phe Thr
145 150 155 160

Ser Trp Val Arg Tyr Ile Gln Tyr Gly Val Tyr Val Val Val Gly Ile
165 170 175

Val Ala Leu Arg Ile Val Ile Tyr Ile Val Gln Met Leu Ser Arg Leu
180 185 190

Arg Lys Gly Tyr Arg Pro Val Phe Ser Ser Pro Pro Gly Tyr Ile Gln
195 200 205

Gln Ile His Ile His Lys Asp Gln Glu Gln Pro Ala Arg Glu Glu Thr
210 215 220

Glu Glu Asp Val Gly Ser Asn Gly Gly Asp Lys Ser Trp Leu
225 230 235

<210> 19
<211> 2427
<212> DNA
<213> HIV-2/VCP Clone p16.9 (env)

<400> 19
atgaaggta gtaagaatca actgctgatt gctattatac tagctagtgc ttacctaaca 60
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ccccctgtttt gtgcaaccaa aaatagagat acttggggaa ccatacagtg cttgccagac 180
aatgatgatt atcagggaaat agctctaaat gtaacagagg ctttcgatgc atgaaataat 240
acagtaacag aacaaggcagt ggaggatgtc tggaaatctat ttgagacatc aataaaacca 300

tgtgtcaaat taacaccctt atgtgttagca atgaactgtta caaggaacat gaccacatcc 360
acagggacca cagacacccca aaatatcaca attataatgc acacttcgccc atgcgtacgt 420
gcagacaact gcacaggatt aaaggaggaa gaaatggtcg actgtcagtt taatatgaca 480
ggatttagaga gagacaagag aaaacagtat actggagcat ggtactcaaa agatgtgatt 540
tgtgacaata acacctaag tcggagcaag ttttacatga accattgcaaa tacatcagtc 600
atcacagagt catgtataa gcactattgg gatgctatga ggtttagata ctgtgcacca 660
ccgggttttgc ccctactaag atgcaatgat actaattatt caggcttgc acctaattgc 720
tctaaagtag tagctgctac atgcaccaga atgatggaaa cgcaatcttc tacatggttt 780
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agaactatta tcagcttaaa taacttttat aatctcacta tgcattgtaa gaggccggga 900
aataagggtg ccggcaaacc caggcaagca tgggttttgt tcaaaggcga atggaaggaa 960
gccatgcagg aggtgaaggaa gacccttgcg aaacatccca gatataaagg gaacaggagc 1020
cgcacagaga atattaaatt taaagcacca ggaagaggct cagacccaga agcagcatac 1080
atgtggacta actgcagagg ggaatttctc tactgcaaca tggcttgggt cctcaattgg 1140
gtagataaca ggacgggtca gaaacagcgc aattatgcac cgtgccatat aaggcaaata 1200
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cagagacata caagaggtgt gttcgtgcta gggttcttgg gtttctcgc aacggcaggt 1500
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ctgaccgtct gggaaactaa aatctccag acaagagtca ctgctataga gaaataccta 1680
aaggaccagg cgcaagttaaa ttcatggga tgtgcgttta gacaagtctg ccacacttct 1740
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gaacagaaaag tccgctactg ggaggcaaat atcagtcaaa gtctagaaca agcacaattt 1860
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tggcttgcact tcacccctg ggtcaggtat attcaatatg gagtttatgt agtagtagga 1980

atagtaactt taagaatagt aatatatata gtacagatgt taagtagact taggaaggc	2040
tataggcctg ttttctcctc cccccccggt tatatccaac agatccatat ccacaaggac	2100
caggaacagc cagccagaga agaaacagaa gaagacgtt gaaagcaacgg tggagacaga	2160
tcttggcttt agccgatagc atatattcat ttcctgatcc gcctgctgat tcgccttgc	2220
atcgggctat acaacatctg cagagactta ctatccagga tctccccat cctccaacca	2280
atcttccaga gtctccagag agcactaaca gcaatcagag actggctgag gcttaagca	2340
gcctacctgc agtatgggtg cgagtggatc caagaagcgt tccaaggccct tgcaaggact	2400
acaagagaga ctcttgcagg cgccgggg	2427

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<210> 20
<211> 1455
<212> DNA
<213> HIV-2/VCP Clone p16.9 (gp120)

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ccccgtttt gtgcaaccaa aaatagagat acttggggaa ccatacagtg cttgccagac	180
aatgatgatt atcagggaaat agctctaaat gtaacagagg ctttcgatgc atgaaataat	240
acagtaacag aacaaggcgt ggaggatgtc tggaaatctat ttgagacatc aataaaacca	300
tgtgtcaaata taacaccctt atgtgttagca atgaactgta caaggaacat gaccacatcc	360
acagggacca cagacacacca aaatatcaca attataaatg acacttcgcc atgcgtacgt	420
gcagacaact gcacaggatt aaaggaggaa gaaatggtcg actgtcagtt taatatgaca	480
ggatttagaga gagacaagag aaaacagtat actggagcat ggtactcaaa agatgtgatt	540
tgtgacaata acacctaag tcggagcaag tgttacatga accattgcaa tacatcagtc	600
atcacagagt catgtataa gcactattgg gatgctatga gtttttagata ctgtgcacca	660
ccgggttttgc ccctactaag atgcaatgt actaattatt caggcttgc acctaattgc	720
tctaaagtat tagctgctac atgcaccaga atgatggaaa cgcaatctc tacatggttt	780
ggatttaatg gcactagagc agaaaataga acatatatct attggcatgg taaaaataac	840
agaactatta tcagctaaa taactttat aatctacta tgcattgtaa gaggccggga	900
aataagggtg ccggcaaacc caggcaagca tgggtttgg tcaaaggcga atgaaaggaa	960
gccatgcagg aggtgaagga gacccttgcg aaacatccca gatataaagg gaacaggagc	1020

cgcacagaga atattaaatt taaagcacca ggaagaggct cagacccaga agcagcatac	1080
atgtggacta actgcagagg ggaatttctc tactgcaaca tggcttgggtt cctcaattgg	1140
gtagataaca ggacgggtca gaaacagcgc aattatgcac cgtccatata aaggcaaata	1200
attaatactt ggcacagggt agggaaaaac atatatttgc ctcccaggga agggagttg	1260
acctgcaact caacagtgc cagcataatt gccaacattt gatcggaga tcaaacagat	1320
attaccttta gtgcagaggt ggcagaacta taccgattgg aattgggaga ttacaaatta	1380
gtagaaatca caccaattgg cttcgcacct acatcagtaa agagatactc ctctgctcac	1440
cagagacata caaga	1455

<210> 21
 <211> 717
 <212> DNA
 <213> HIV-2/VCP Clone p16.9 (gp41)

<400> 21	
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gcgtcggtga cgctgaccgc ccagtccgg acttcattgg ctggatagt gcagcaacag	120
caacagctgt tggacgtggt caagaaacaa caagaaatgt tgcaactgac cgtctggga	180
actaaaaatc tccagacaag agtcactgct atagagaaat acctaaagga ccaggcgcag	240
ttaaattcat gggatgtgc gtttagacaa gtctgccaca cttctgtacc atggtaaat	300
gatagcttga cacctgattt gaacaatatg acgtggcagg aatggaaaca gaaagtccgc	360
tactgggagg caaatatcag tcaaagtcta gaacaagcac aaattcagca agaaaagaat	420
ttgtatgagc tgcaaaaatt aaatagctgg ggtgtttta ccaattggct tgacttcacc	480
tcctgggtca ggtatattca atatggagtt tatgttagtag taggaatagt aactttaaga	540
atagtaatat atatagtaca gatgttaagt agacttagga agggctatacg gcctgtttc	600
tcctcccccc ccggttatat ccaacagatc catatccaca aggaccagga acagccagcc	660
agagaagaaa cagaagaaga cgttggaaagc aacggtgag acagatctg gctttag	717

<210> 22
 <211> 723
 <212> PRT
 <213> HIV-2/VCP Clone p16.9 (env)

<400> 22

Met Lys Gly Ser Lys Asn Gln Leu Leu Ile Ala Ile Ile Leu Ala Ser			
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Ala Tyr Leu Thr His Cys Lys Gln Phe Val Thr Val Phe Tyr Gly Ile
20 25 30

Pro Ala Trp Arg Asn Ala Ser Ile Pro Leu Phe Cys Ala Thr Lys Asn
35 40 45

Arg Asp Thr Trp Gly Thr Ile Gln Cys Leu Pro Asp Asn Asp Asp Tyr
50 55 60

Gln Glu Ile Ala Leu Asn Val Thr Glu Ala Phe Asp Ala Trp Asn Asn
65 70 75 80

Thr Val Thr Glu Gln Ala Val Glu Asp Val Trp Asn Leu Phe Glu Thr
85 90 95

Ser Ile Lys Pro Cys Val Lys Leu Thr Pro Leu Cys Val Ala Met Asn
100 105 110

Cys Thr Arg Asn Met Thr Thr Ser Thr Gly Thr Thr Asp Thr Gln Asn
115 120 125

Ile Thr Ile Ile Asn Asp Thr Ser Pro Cys Val Arg Ala Asp Asn Cys
130 135 140

Thr Gly Leu Lys Glu Glu Glu Met Val Asp Cys Gln Phe Asn Met Thr
145 150 155 160

Gly Leu Glu Arg Asp Lys Arg Lys Gln Tyr Thr Gly Ala Trp Tyr Ser
165 170 175

Lys Asp Val Ile Cys Asp Asn Asn Thr Ser Ser Arg Ser Lys Cys Tyr
180 185 190

Met Asn His Cys Asn Thr Ser Val Ile Thr Glu Ser Cys Asp Lys His
195 200 205

Tyr Trp Asp Ala Met Arg Phe Arg Tyr Cys Ala Pro Pro Gly Phe Ala
210 215 220

Leu Leu Arg Cys Asn Asp Thr Asn Tyr Ser Gly Phe Ala Pro Asn Cys
225 230 235 240

Ser Lys Val Val Ala Ala Thr Cys Thr Arg Met Met Glu Thr Gln Ser
245 250 255

Ser Thr Trp Phe Gly Phe Asn Gly Thr Arg Ala Glu Asn Arg Thr Tyr
260 265 270

Ile Tyr Trp His Gly Lys Asn Asn Arg Thr Ile Ile Ser Leu Asn Asn
275 280 285

Phe Tyr Asn Leu Thr Met His Cys Lys Arg Pro Gly Asn Lys Gly Ala
290 295 300

Gly Lys Pro Arg Gln Ala Trp Cys Trp Phe Lys Gly Glu Trp Lys Glu
305 310 315 320

Ala Met Gln Glu Val Lys Glu Thr Leu Ala Lys His Pro Arg Tyr Lys
325 330 335

Gly Asn Arg Ser Arg Thr Glu Asn Ile Lys Phe Lys Ala Pro Gly Arg
340 345 350

Gly Ser Asp Pro Glu Ala Ala Tyr Met Trp Thr Asn Cys Arg Gly Glu
355 360 365

Phe Leu Tyr Cys Asn Met Ala Trp Phe Leu Asn Trp Val Asp Asn Arg
370 375 380

Thr Gly Gln Lys Gln Arg Asn Tyr Ala Pro Cys His Ile Arg Gln Ile
385 390 395 400

Ile Asn Thr Trp His Arg Val Gly Lys Asn Ile Tyr Leu Pro Pro Arg
405 410 415

Glu Gly Glu Leu Thr Cys Asn Ser Thr Val Thr Ser Ile Ile Ala Asn
420 425 430

Ile Asp Thr Gly Asp Gln Thr Asp Ile Thr Phe Ser Ala Glu Val Ala
435 440 445

Glu Leu Tyr Arg Leu Glu Leu Gly Asp Tyr Lys Leu Val Glu Ile Thr
450 455 460

Pro Ile Gly Phe Ala Pro Thr Ser Val Lys Arg Tyr Ser Ser Ala His
465 470 475 480

Gln Arg His Thr Arg Gly Val Phe Val Leu Gly Phe Leu Gly Phe Leu
485 490 495

Ala Thr Ala Gly Ser Ala Met Gly Ala Ala Ser Val Thr Leu Thr Ala
500 505 510

Gln Ser Arg Thr Ser Leu Ala Gly Ile Val Gln Gln Gln Gln Leu
515 520 525

Leu Asp Val Val Lys Lys Gln Gln Glu Met Leu Arg Leu Thr Val Trp
530 535 540

Gly Thr Lys Asn Leu Gln Thr Arg Val Thr Ala Ile Glu Lys Tyr Leu
545 550 555 560

Lys Asp Gln Ala Gln Leu Asn Ser Trp Gly Cys Ala Phe Arg Gln Val
565 570 575

Cys His Thr Ser Val Pro Trp Val Asn Asp Ser Leu Thr Pro Asp Trp
580 585 590

Asn Asn Met Thr Trp Gln Glu Trp Glu Gln Lys Val Arg Tyr Trp Glu
595 600 605

Ala Asn Ile Ser Gln Ser Leu Glu Gln Ala Gln Ile Gln Gln Glu Lys
610 615 620

Asn Leu Tyr Glu Leu Gln Lys Leu Asn Ser Trp Gly Val Phe Thr Asn
625 630 635 640

Trp Leu Asp Phe Thr Ser Trp Val Arg Tyr Ile Gln Tyr Gly Val Tyr
645 650 655

Val Val Val Gly Ile Val Thr Leu Arg Ile Val Ile Tyr Ile Val Gln
660 665 670

Met Leu Ser Arg Leu Arg Lys Gly Tyr Arg Pro Val Phe Ser Ser Pro
675 680 685

Pro Gly Tyr Ile Gln Gln Ile His Ile His Lys Asp Gln Glu Gln Pro

690

695

700

Ala Arg Glu Glu Thr Glu Glu Asp Val Gly Ser Asn Gly Gly Asp Arg
705 710 715 720

Ser Trp Leu

<210> 23
<211> 485
<212> PRT
<213> HIV-2/VCP Clone p16.9 (gp120)

<400> 23

Met Lys Gly Ser Lys Asn Gln Leu Leu Ile Ala Ile Ile Leu Ala Ser
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Ala Tyr Leu Thr His Cys Lys Gln Phe Val Thr Val Phe Tyr Gly Ile
20 25 30

Pro Ala Trp Arg Asn Ala Ser Ile Pro Leu Phe Cys Ala Thr Lys Asn
35 40 45

Arg Asp Thr Trp Gly Thr Ile Gln Cys Leu Pro Asp Asn Asp Asp Tyr
50 55 60

Gln Glu Ile Ala Leu Asn Val Thr Glu Ala Phe Asp Ala Trp Asn Asn
65 70 75 80

Thr Val Thr Glu Gln Ala Val Glu Asp Val Trp Asn Leu Phe Glu Thr
85 90 95

Ser Ile Lys Pro Cys Val Lys Leu Thr Pro Leu Cys Val Ala Met Asn
100 105 110

Cys Thr Arg Asn Met Thr Thr Ser Thr Gly Thr Thr Asp Thr Gln Asn
115 120 125

Ile Thr Ile Ile Asn Asp Thr Ser Pro Cys Val Arg Ala Asp Asn Cys
130 135 140

Thr Gly Leu Lys Glu Glu Glu Met Val Asp Cys Gln Phe Asn Met Thr
145 150 155 160

Gly Leu Glu Arg Asp Lys Arg Lys Gln Tyr Thr Gly Ala Trp Tyr Ser
165 170 175

Lys Asp Val Ile Cys Asp Asn Asn Thr Ser Ser Arg Ser Lys Cys Tyr
180 185 190

Met Asn His Cys Asn Thr Ser Val Ile Thr Glu Ser Cys Asp Lys His
195 200 205

Tyr Trp Asp Ala Met Arg Phe Arg Tyr Cys Ala Pro Pro Gly Phe Ala
210 215 220

Leu Leu Arg Cys Asn Asp Thr Asn Tyr Ser Gly Phe Ala Pro Asn Cys
225 230 235 240

Ser Lys Val Val Ala Ala Thr Cys Thr Arg Met Met Glu Thr Gln Ser
245 250 255

Ser Thr Trp Phe Gly Phe Asn Gly Thr Arg Ala Glu Asn Arg Thr Tyr
260 265 270

Ile Tyr Trp His Gly Lys Asn Asn Arg Thr Ile Ile Ser Leu Asn Asn
275 280 285

Phe Tyr Asn Leu Thr Met His Cys Lys Arg Pro Gly Asn Lys Gly Ala
290 295 300

Gly Lys Pro Arg Gln Ala Trp Cys Trp Phe Lys Gly Glu Trp Lys Glu
305 310 315 320

Ala Met Gln Glu Val Lys Glu Thr Leu Ala Lys His Pro Arg Tyr Lys
325 330 335

Gly Asn Arg Ser Arg Thr Glu Asn Ile Lys Phe Lys Ala Pro Gly Arg
340 345 350

Gly Ser Asp Pro Glu Ala Ala Tyr Met Trp Thr Asn Cys Arg Gly Glu
355 360 365

Phe Leu Tyr Cys Asn Met Ala Trp Phe Leu Asn Trp Val Asp Asn Arg
370 375 380

Thr Gly Gln Lys Gln Arg Asn Tyr Ala Pro Cys His Ile Arg Gln Ile
385 390 395 400

Ile Asn Thr Trp His Arg Val Gly Lys Asn Ile Tyr Leu Pro Pro Arg
405 410 415

Glu Gly Glu Leu Thr Cys Asn Ser Thr Val Thr Ser Ile Ile Ala Asn
420 425 430

Ile Asp Thr Gly Asp Gln Thr Asp Ile Thr Phe Ser Ala Glu Val Ala
435 440 445

Glu Leu Tyr Arg Leu Glu Leu Gly Asp Tyr Lys Leu Val Glu Ile Thr
450 455 460

Pro Ile Gly Phe Ala Pro Thr Ser Val Lys Arg Tyr Ser Ser Ala His
465 470 475 480

Gln Arg His Thr Arg
485

<210> 24
<211> 238
<212> PRT
<213> HIV-2/VCP Clone p16.9 (gp41)

<400> 24

Gly Val Phe Val Leu Gly Phe Leu Gly Phe Leu Ala Thr Ala Gly Ser
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Ala Met Gly Ala Ala Ser Val Thr Leu Thr Ala Gln Ser Arg Thr Ser
20 25 30

Leu Ala Gly Ile Val Gln Gln Gln Gln Leu Leu Asp Val Val Lys
35 40 45

Lys Gln Gln Glu Met Leu Arg Leu Thr Val Trp Gly Thr Lys Asn Leu
50 55 60

Gln Thr Arg Val Thr Ala Ile Glu Lys Tyr Leu Lys Asp Gln Ala Gln
65 70 75 80

Leu Asn Ser Trp Gly Cys Ala Phe Arg Gln Val Cys His Thr Ser Val
85 90 95

Pro Trp Val Asn Asp Ser Leu Thr Pro Asp Trp Asn Asn Met Thr Trp
100 105 110

Gln Glu Trp Glu Gln Lys Val Arg Tyr Trp Glu Ala Asn Ile Ser Gln
115 120 125

Ser Leu Glu Gln Ala Gln Ile Gln Gln Glu Lys Asn Leu Tyr Glu Leu
130 135 140

Gln Lys Leu Asn Ser Trp Gly Val Phe Thr Asn Trp Leu Asp Phe Thr
145 150 155 160

Ser Trp Val Arg Tyr Ile Gln Tyr Gly Val Tyr Val Val Val Gly Ile
165 170 175

Val Thr Leu Arg Ile Val Ile Tyr Ile Val Gln Met Leu Ser Arg Leu
180 185 190

Arg Lys Gly Tyr Arg Pro Val Phe Ser Ser Pro Pro Gly Tyr Ile Gln
195 200 205

Gln Ile His Ile His Lys Asp Gln Glu Gln Pro Ala Arg Glu Glu Thr
210 215 220

Glu Glu Asp Val Gly Ser Asn Gly Gly Asp Arg Ser Trp Leu
225 230 235

<210> 25
<211> 2142
<212> DNA
<213> HIV-2/VCP Clone 8c.3 (env)

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ccccctgtttt gtgcaaccaa aaatagagat acttggggaa ccatacagtg cttgccagac 180
aatgatgatt atcagggaaat agctctaaat gtaacagagg ctttcgatgc atgaaataat 240
acagtaacag aacaaggcagt ggaggatgtc tggaatctat ttgagacatc aataaaacca 300
tgtgtcaaat taacaccctt atgtgttagca atgaactgta caaggaacat gaccacatcc 360
acagggacca cagacacccca aaatatcaca attataaattg acacttcgcc atgcgtacgt 420

gcagacaact gcacaggatt aaaggaggaa gaaatggtcg actgtcagtt taatatgaca	480
ggatttagaga gagacaagag aaaacagtat actggaacat ggtactcaaa agatgtgatt	540
tgtgacaata acacctaag tcggagcaag tgttacatga accattgcaa tacatcagtc	600
atcacaaagt catgtgataa gcactattgg gatgctatga ggtagata ctgtgcacca	660
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agaactatta tcagctaaa taacttttat aatctacta tgcattgtaa ggggccggc	900
tgggtttggc tcaaaggcga atggaaggaa gccatgcagg aggtgaagga gacccttgcg	960
aaacatccca gatataaagg gaacaggagc cgcacagaga atattaaatt taaagcacca	1020
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tactgcaaca tggcttggc cctcaactgg gtagataaca ggacgggtcg gaaacagcgc	1140
aattatgcac cgtccatata aaggcaaata attaatactt ggcacagggt agggaaaaac	1200
atatatggc cttccaggaa agggagtttgcctgcaact caacagtgc cagcataattt	1260
gccaacatttgc atacgggaga tcaaacagat attacctta gtgcagagg ggcagaacta	1320
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tgtgcgttta gacaagtctg ccacacttct gtaccatgg taaatgatag cttgacac	1740
gattggaaaca atatgacgtg gcaggaatgg gaacagaaag tccgctactg ggaggcaa	1800
atcagtcaaa gtctagaaca agcacaattt cagcaagaaa agaatttgc tgagctgca	1860
aaattaaata gctgggtgt ttttaccaat tggcttgact tcacccctg ggtcaggtat	1920
attcaatatg gagcatatgt agtagtagga atagtaactt taagaatagt aatataata	1980
gtacagatgt taagtagact taggaaggc tataggcctg ttttctcctc cccccccggt	2040
tatatccaac agatccatata ccacaaggac caggaacagc cagccagaga agaaacagaa	2100

gaagacgttg gaagcaacgg tggagacaga tcttggcttt ag 2142

<210> 26
<211> 1425
<212> DNA
<213> HIV-2/VCP Clone 8c.3 (gp120)

<400> 26
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ccccctgtttt gtgcaaccaa aaatagagat acttggggaa ccatacagtg cttgccagac 180
aatgatgatt atcaggaaat agctctaaat gtaacagagg ctttcgatgc atggaataat 240
acagtaacag aacaaggcagt ggaggatgtc tggaaatctat ttgagacatc aataaaacca 300
tgtgtcaaattt taacaccctt atgtgttagca atgaactgta caaggaacat gaccacatcc 360
acagggacca cagacacccca aaatatcaca attataaatg acacttcgcc atgcgtacgt 420
gcagacaact gcacaggatt aaaggagggaa gaaatggtcg actgtcagtt taatatgaca 480
ggatttagaga gagacaagag aaaacagtat actggaacat ggtactcaa agatgtgatt 540
tgtgacaata acacctaag tcggagcaag tgttacatga accattgcaa tacatcagtc 600
atcacaaagt catgtgataa gcactattgg gatgctatga ggttttagata ctgtgcacca 660
ccgggttttgc ccctactaag atgcaatgat actaattatt caggcttgc acctaattgc 720
tctaaagtag tagctgctac atgcaccaga atgatggaaa cgcaatcttc tacatggttt 780
ggatTTAATG gcactagagc agaaaataga acatatatattt attggcatgg taaaaataac 840
agaactatta tcagcttaaa taacttttat aatctcacta tgcattgtaa gggtgccggc 900
tgggtttggc tcaaaggcga atggaaggaa gccatgcagg aggtgaaggaa gacccttgcg 960
aaacatccca gatataaagg gaacaggagc cgcacagaga atattaaatt taaagcacca 1020
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tactgcaaca tggcttgggtt cctcaactgg gtagataaca ggacgggtcg gaaacagcgc 1140
aattatgcac cgtgccatat aaggcaaata attaatactt ggcacagggtt agggaaaaac 1200
atataatttgc ctcccaggaa aggggagttg gcctgcaact caacagtgcac cagcataatt 1260
gccaacatttgc atacgggaga tcaaacagat attacctta gtgcagaggtt ggcagaacta 1320
taccgattgg aattgggaga ttacaaatca gtagaaatca caccaattgg cttcgacact 1380
acatcagtaa agagatactc ctctgctcac cagagacata caaga 1425

<210> 27
<211> 717
<212> DNA
<213> HIV-2/VCP Clone 8c.3 (gp41)

<400> 27
ggtgtgttcg tgcttagggtt cttgggtttt ctcgcaacgg caggttctgc aatgggcgcg 60
gcgtcggtga cgctgaccgc ccagtcggc acttcattgg ctgggatagt gcagcaacag 120
caacagctgt tggacgtggt caagaaacaa caagaaatgt tgcgactgac cgtctgggga 180
actaaaaatc tccagacaag agtcactgct atagagaaat acctaaagga ccaggcgcag 240
ttaaattcat gggatgtgc gtttagacaa gtctgccaca cttctgtacc atggtaaat 300
gatacgcttga cacctgatttgaacaatatg acgtggcagg aatggaaaca gaaagtccgc 360
tactgggagg caaatatcag tcaaagtcta gaacaagcac aaattcagca agaaaagaat 420
ttgtatgagc tgcaaaaatt aaatagctgg ggtgtttta ccaattggct tgacttcacc 480
tcctgggtca ggtatattca atatggagca tatgttagtag taggaatagt aactttaaga 540
atagtaatat atatagtaca gatgttaagt agacttagga agggctatacg gcctgtttc 600
tcctcccccc ccggttatat ccaacagatc catatccaca aggaccagga acagccagcc 660
agagaagaaa cagaagaaga cgttggaaagc aacggtggag acagatcttgcgttt 717

<210> 28
<211> 713
<212> PRT
<213> HIV-2/VCP Clone 8c.3 (env)

<400> 28

Met Lys Gly Ser Lys Asn Gln Leu Leu Ile Ala Ile Ile Leu Ala Ser
1 5 10 15

Ala Tyr Leu Thr His Cys Lys Gln Phe Val Thr Val Phe Tyr Gly Ile
20 25 30

Pro Ala Trp Arg Asn Ala Ser Ile Pro Leu Phe Cys Ala Thr Lys Asn
35 40 45

Arg Asp Thr Trp Gly Thr Ile Gln Cys Leu Pro Asp Asn Asp Asp Tyr
50 55 60

Gln Glu Ile Ala Leu Asn Val Thr Glu Ala Phe Asp Ala Trp Asn Asn
65 70 75 80

Thr Val Thr Glu Gln Ala Val Glu Asp Val Trp Asn Leu Phe Glu Thr
85 90 95

Ser Ile Lys Pro Cys Val Lys Leu Thr Pro Leu Cys Val Ala Met Asn
100 105 110

Cys Thr Arg Asn Met Thr Thr Ser Thr Gly Thr Thr Asp Thr Gln Asn
115 120 125

Ile Thr Ile Ile Asn Asp Thr Ser Pro Cys Val Arg Ala Asp Asn Cys
130 135 140

Thr Gly Leu Lys Glu Glu Glu Met Val Asp Cys Gln Phe Asn Met Thr
145 150 155 160

Gly Leu Glu Arg Asp Lys Arg Lys Gln Tyr Thr Gly Thr Trp Tyr Ser
165 170 175

Lys Asp Val Ile Cys Asp Asn Asn Thr Ser Ser Arg Ser Lys Cys Tyr
180 185 190

Met Asn His Cys Asn Thr Ser Val Ile Thr Lys Ser Cys Asp Lys His
195 200 205

Tyr Trp Asp Ala Met Arg Phe Arg Tyr Cys Ala Pro Pro Gly Phe Ala
210 215 220

Leu Leu Arg Cys Asn Asp Thr Asn Tyr Ser Gly Phe Ala Pro Asn Cys
225 230 235 240

Ser Lys Val Val Ala Ala Thr Cys Thr Arg Met Met Glu Thr Gln Ser
245 250 255

Ser Thr Trp Phe Gly Phe Asn Gly Thr Arg Ala Glu Asn Arg Thr Tyr
260 265 270

Ile Tyr Trp His Gly Lys Asn Asn Arg Thr Ile Ile Ser Leu Asn Asn
275 280 285

Phe Tyr Asn Leu Thr Met His Cys Lys Gly Ala Gly Trp Cys Trp Phe
290 295 300

Lys Gly Glu Trp Lys Glu Ala Met Gln Glu Val Lys Glu Thr Leu Ala
305 310 315 320

Lys His Pro Arg Tyr Lys Gly Asn Arg Ser Arg Thr Glu Asn Ile Lys
325 330 335

Phe Lys Ala Pro Gly Arg Gly Ser Asp Pro Glu Ala Ala Tyr Met Trp
340 345 350

Thr Asn Cys Arg Gly Glu Phe Leu Tyr Cys Asn Met Ala Trp Phe Leu
355 360 365

Asn Trp Val Asp Asn Arg Thr Gly Arg Lys Gln Arg Asn Tyr Ala Pro
370 375 380

Cys His Ile Arg Gln Ile Ile Asn Thr Trp His Arg Val Gly Lys Asn
385 390 395 400

Ile Tyr Leu Pro Pro Arg Glu Gly Glu Leu Ala Cys Asn Ser Thr Val
405 410 415

Thr Ser Ile Ile Ala Asn Ile Asp Thr Gly Asp Gln Thr Asp Ile Thr
420 425 430

Phe Ser Ala Glu Val Ala Glu Leu Tyr Arg Leu Glu Leu Gly Asp Tyr
435 440 445

Lys Leu Val Glu Ile Thr Pro Ile Gly Phe Ala Pro Thr Ser Val Lys
450 455 460

Arg Tyr Ser Ser Ala His Gln Arg His Thr Arg Gly Val Phe Val Leu
465 470 475 480

Gly Phe Leu Gly Phe Leu Ala Thr Ala Gly Ser Ala Met Gly Ala Ala
485 490 495

Ser Val Thr Leu Thr Ala Gln Ser Arg Thr Ser Leu Ala Gly Ile Val
500 505 510

Gln Gln Gln Gln Leu Leu Asp Val Val Lys Lys Gln Gln Glu Met
515 520 525

Leu Arg Leu Thr Val Trp Gly Thr Lys Asn Leu Gln Thr Arg Val Thr
530 535 540

Ala Ile Glu Lys Tyr Leu Lys Asp Gln Ala Gln Leu Asn Ser Trp Gly
545 550 555 560

Cys Ala Phe Arg Gln Val Cys His Thr Ser Val Pro Trp Val Asn Asp
565 570 575

Ser Leu Thr Pro Asp Trp Asn Asn Met Thr Trp Gln Glu Trp Glu Gln
580 585 590

Lys Val Arg Tyr Trp Glu Ala Asn Ile Ser Gln Ser Leu Glu Gln Ala
595 600 605

Gln Ile Gln Gln Glu Lys Asn Leu Tyr Glu Leu Gln Lys Leu Asn Ser
610 615 620

Trp Gly Val Phe Thr Asn Trp Leu Asp Phe Thr Ser Trp Val Arg Tyr
625 630 635 640

Ile Gln Tyr Gly Ala Tyr Val Val Val Gly Ile Val Thr Leu Arg Ile
645 650 655

Val Ile Tyr Ile Val Gln Met Leu Ser Arg Leu Arg Lys Gly Tyr Arg
660 665 670

Pro Val Phe Ser Ser Pro Pro Gly Tyr Ile Gln Gln Ile His Ile His
675 680 685

Lys Asp Gln Glu Gln Pro Ala Arg Glu Glu Thr Glu Glu Asp Val Gly
690 695 700

Ser Asn Gly Gly Asp Arg Ser Trp Leu
705 710

<210> 29
<211> 475
<212> PRT
<213> HIV-2/VCP Clone 8c.3 (gp120)

<400> 29

Met Lys Gly Ser Lys Asn Gln Leu Leu Ile Ala Ile Ile Leu Ala Ser
1 5 10 15

Ala Tyr Leu Thr His Cys Lys Gln Phe Val Thr Val Phe Tyr Gly Ile
20 25 30

Pro Ala Trp Arg Asn Ala Ser Ile Pro Leu Phe Cys Ala Thr Lys Asn
35 40 45

Arg Asp Thr Trp Gly Thr Ile Gln Cys Leu Pro Asp Asn Asp Asp Tyr
50 55 60

Gln Glu Ile Ala Leu Asn Val Thr Glu Ala Phe Asp Ala Trp Asn Asn
65 70 75 80

Thr Val Thr Glu Gln Ala Val Glu Asp Val Trp Asn Leu Phe Glu Thr
85 90 95

Ser Ile Lys Pro Cys Val Lys Leu Thr Pro Leu Cys Val Ala Met Asn
100 105 110

Cys Thr Arg Asn Met Thr Thr Ser Thr Gly Thr Thr Asp Thr Gln Asn
115 120 125

Ile Thr Ile Ile Asn Asp Thr Ser Pro Cys Val Arg Ala Asp Asn Cys
130 135 140

Thr Gly Leu Lys Glu Glu Glu Met Val Asp Cys Gln Phe Asn Met Thr
145 150 155 160

Gly Leu Glu Arg Asp Lys Arg Lys Gln Tyr Thr Gly Thr Trp Tyr Ser
165 170 175

Lys Asp Val Ile Cys Asp Asn Asn Thr Ser Ser Arg Ser Lys Cys Tyr
180 185 190

Met Asn His Cys Asn Thr Ser Val Ile Thr Lys Ser Cys Asp Lys His
195 200 205

Tyr Trp Asp Ala Met Arg Phe Arg Tyr Cys Ala Pro Pro Gly Phe Ala
210 215 220

Leu Leu Arg Cys Asn Asp Thr Asn Tyr Ser Gly Phe Ala Pro Asn Cys
225 230 235 240

Ser Lys Val Val Ala Ala Thr Cys Thr Arg Met Met Glu Thr Gln Ser
245 250 255

Ser Thr Trp Phe Gly Phe Asn Gly Thr Arg Ala Glu Asn Arg Thr Tyr
260 265 270

Ile Tyr Trp His Gly Lys Asn Asn Arg Thr Ile Ile Ser Leu Asn Asn
275 280 285

Phe Tyr Asn Leu Thr Met His Cys Lys Gly Ala Gly Trp Cys Trp Phe
290 295 300

Lys Gly Glu Trp Lys Glu Ala Met Gln Glu Val Lys Glu Thr Leu Ala
305 310 315 320

Lys His Pro Arg Tyr Lys Gly Asn Arg Ser Arg Thr Glu Asn Ile Lys
325 330 335

Phe Lys Ala Pro Gly Arg Gly Ser Asp Pro Glu Ala Ala Tyr Met Trp
340 345 350

Thr Asn Cys Arg Gly Glu Phe Leu Tyr Cys Asn Met Ala Trp Phe Leu
355 360 365

Asn Trp Val Asp Asn Arg Thr Gly Arg Lys Gln Arg Asn Tyr Ala Pro
370 375 380

Cys His Ile Arg Gln Ile Ile Asn Thr Trp His Arg Val Gly Lys Asn
385 390 395 400

Ile Tyr Leu Pro Pro Arg Glu Gly Glu Leu Ala Cys Asn Ser Thr Val
405 410 415

Thr Ser Ile Ile Ala Asn Ile Asp Thr Gly Asp Gln Thr Asp Ile Thr
420 425 430

Phe Ser Ala Glu Val Ala Glu Leu Tyr Arg Leu Glu Leu Gly Asp Tyr
435 440 445

Lys Leu Val Glu Ile Thr Pro Ile Gly Phe Ala Pro Thr Ser Val Lys
450 455 460

Arg Tyr Ser Ser Ala His Gln Arg His Thr Arg
465 470 475

<210> 30
<211> 238
<212> PRT
<213> HIV-2/VCP Clone 8c.3 (gp41)

<400> 30

Gly Val Phe Val Leu Gly Phe Leu Gly Phe Leu Ala Thr Ala Gly Ser
1 5 10 15

Ala Met Gly Ala Ala Ser Val Thr Leu Thr Ala Gln Ser Arg Thr Ser
20 25 30

Leu Ala Gly Ile Val Gln Gln Gln Gln Leu Leu Asp Val Val Lys
35 40 45

Lys Gln Gln Glu Met Leu Arg Leu Thr Val Trp Gly Thr Lys Asn Leu
50 55 60

Gln Thr Arg Val Thr Ala Ile Glu Lys Tyr Leu Lys Asp Gln Ala Gln
65 70 75 80

Leu Asn Ser Trp Gly Cys Ala Phe Arg Gln Val Cys His Thr Ser Val
85 90 95

Pro Trp Val Asn Asp Ser Leu Thr Pro Asp Trp Asn Asn Met Thr Trp
100 105 110

Gln Glu Trp Glu Gln Lys Val Arg Tyr Trp Glu Ala Asn Ile Ser Gln
115 120 125

Ser Leu Glu Gln Ala Gln Ile Gln Gln Glu Lys Asn Leu Tyr Glu Leu
130 135 140

Gln Lys Leu Asn Ser Trp Gly Val Phe Thr Asn Trp Leu Asp Phe Thr
145 150 155 160

Ser Trp Val Arg Tyr Ile Gln Tyr Gly Ala Tyr Val Val Val Gly Ile
165 170 175

Val Thr Leu Arg Ile Val Ile Tyr Ile Val Gln Met Leu Ser Arg Leu
180 185 190

Arg Lys Gly Tyr Arg Pro Val Phe Ser Ser Pro Pro Gly Tyr Ile Gln
195 200 205

Gln Ile His Ile His Lys Asp Gln Glu Gln Pro Ala Arg Glu Glu Thr
210 215 220

Glu Glu Asp Val Gly Ser Asn Gly Gly Asp Arg Ser Trp Leu
225 230 235